GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2005, 09:37:08 ; Search time 11131 Seconds
                                        (without alignments)
                                        11583.805 Million cell updates/sec

Title: US-10-039-272-1
Perfect score: 2661
Sequence: 1 cggcacgagggcccagagga.........aaaaaaaaaaaaaaaaaaaa 2661

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                   1: gb_ba:*
                   2: gb_htg:*
                   3: gb_in:*
                   4: gb_om:*
                   5: gb_ov:*
                   6: gb_pat:*
                   7: gb_ph:*
                   8: gb_pl:*
                   9: gb_pr:*
                   10: gb_ro:*
                   11: gb_sts:*
                   12: gb_sy:*
                   13: gb_un:*
                   14: gb_vi:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                                    SUMMARIES
                         %
Result   Query
    No.   Score   Match Length DB   ID   Description
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      1   2650   99.6   2662   9   AF322909   AF322909 Homo sapi
      2   2547.8   95.7   2669   6   AR018808   AR018808 Sequence
      3   2547.8   95.7   2669   6   AR018814   AR018814 Sequence

4	2547.8	95.7	2669	6	CQ776677	CQ776677 Sequence
5	2547.8	95.7	2669	6	AX818137	AX818137 Sequence
6	2547.8	95.7	2669	9	HSNMB	X76534 H.sapiens N
7	2533.6	95.2	2658	6	CQ727007	CQ727007 Sequence
8	2522	94.8	2787	9	BC032783	BC032783 Homo sapi
9	2485	93.4	2683	6	AX358788	AX358788 Sequence
10	2485	93.4	2683	6	AX362281	AX362281 Sequence
11	2485	93.4	2683	9	AY359124	AY359124 Homo sapi
12	1671	62.8	1683	6	AX677738	AX677738 Sequence
13	1051.2	39.5	2282	10	BC061725	BC061725 Rattus no
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15	1051.2	39.5	2303	6	BD062749	BD062749 Modulator
16	1049.8	39.5	2279	10	AF322054	AF322054 Mus muscu
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21	1045	39.3	2305	6	CQ777541	CQ777541 Sequence
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23	1002.6	37.7	169739	9	AC005082	AC005082 Homo sapi
c 24	988.2	37.1	221255	9	AC145883	AC145883 Pan trogl
25	854.2	32.1	898	11	G26743	G26743 human STS S
26	673.6	25.3	820	6	CQ427083	CQ427083 Sequence
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28	572	21.5	1690	9	BC011595	BC011595 Homo sapi
29	568.8	21.4	1593	9	HSA505015	AJ505015 Homo sapi
30	546.4	20.5	621	9	BT007074	BT007074 Homo sapi
31	546.4	20.5	621	12	BT007499	BT007499 Synthetic
32	545.6	20.5	619	6	AR176427	AR176427 Sequence
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34	545.6	20.5	619	6	BD226053	BD226053 Compound
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36	545.6	20.5	619	6	BD275724	BD275724 COMPOUNDS
37	545.6	20.5	619	6	AR220496	AR220496 Sequence
38	545.6	20.5	619	6	AR220509	AR220509 Sequence
39	545.6	20.5	619	6	AR255490	AR255490 Sequence
40	545.6	20.5	619	6	AR255503	AR255503 Sequence
41	545.6	20.5	619	6	AR281060	AR281060 Sequence
42	545.6	20.5	619	6	AR281073	AR281073 Sequence
43	545.6	20.5	619	6	AR437851	AR437851 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS   AF322909   2662 bp   mRNA   linear   PRI 23-APR-2003
DEFINITION   Homo sapiens transmembrane glycoprotein HGFIN mRNA, complete cds.
ACCESSION   AF322909
VERSION   AF322909.1 GI:11993664
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1  (bases 1 to 2662)
  AUTHORS     Bandari,P.S., Qian,J., Yehia,G., Joshi,D.D., Maloof,P.B.,
    .         Potian,J., Oh,H.S., Gascon,P., Harrison,J.S. and Rameshwar,P.
    TITLE     Hematopoietic growth factor inducible neurokinin-1 type: a
              transmembrane protein that is similar to neurokinin 1 interacts
              with substance P
  JOURNAL     Regul. Pept. 111 (1-3), 169-178 (2003)
  MEDLINE     22498106
   PUBMED     12609765
REFERENCE     2  (bases 1 to 2662)
  AUTHORS     Rameshwar,P.
    TITLE     Direct Submission
  JOURNAL     Submitted (20-NOV-2000) Medicine, UMDNJ-New Jersey Medical School,
              185 South Orange Ave, MSB, Rm. E-579, Newark, NJ 07103, USA
FEATURES              Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /protein_id="AAG42839.1"
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                     /translation="MECLYYFLGFLLLAARLPLDAAKRFHDVLGNERPSAYMREHNQL
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                     AYVPIAQVKDVYVVTDQIPVFVTMFQKNDRNSSDETFLKDLPIMFDVLIHDPSHFLNY
                     STINYKWSFGDNTGLFVSTNHTVNHTYVLNGTFSLNLTVKAAAPGPCPPPPPPPRPSK
                     PTPSLGPAGDNPLELSRIPDENCQINRYGHFQATITIVEGILEVNIIQMTDVLMPVPW
                     PESSLIDFVVTCQGSIPTEVCTIISDPTCEITQNTVCSPVDVDEMCLLTVRRTFNGSG
                     TYCVNLTLGDDTSLALTSTLISVPDRDPASPLRMANSALISVGCLAIFVTVISLLVYK
                     KHKEYNPIENSPGNVVRSKGLSVFLNRAKAVFFPGNQEKDPLLKNQEFKGVS"
ORIGIN

    Query Match             99.6%;  Score 2650;  DB 9;  Length 2662;
    Best Local Similarity   100.0%;  Pred. No. 0;
    Matches 2661;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         1 CGGCACGAGGGCCCAGAGGAATAAGTTAACCTTGGTGCCTGCGTCCGTGAGAATTCAGCA 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 CGGCACGAGGGCCCAGAGGAATAAGTTAACCTTGGTGCCTGCGTCCGTGAGAATTCAGCA 60


Qy        61 TGGAATGTCTCTACTATTTCCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGATG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 TGGAATGTCTCTACTATTTCCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGATG 120


Qy       121 CCGCCAAACGATTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAGC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CCGCCAAACGATTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAGC 180


Qy       181 ACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAAACTCTACCCAG 240
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Db      181 ACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAAACTCTACCCAG 240

Qy      241 TGTGGAAGCGGGGAGACATGAGGTGGAAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGG 300
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Db      241 TGTGGAAGCGGGGAGACATGAGGTGGAAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGG 300

Qy      301 TCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTGA 360
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 TCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTGA 360

Qy      361 TATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGCA 420
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 TATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGCA 420

Qy      421 GAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACTGGACAGCATGGTCAGAGG 480
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Db      421 GAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACTGGACAGCATGGTCAGAGG 480

Qy      481 ACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAAC 540
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Db      481 ACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAAC 540

Qy      541 CTTTTCCTCACCACCCCGGATGGAGAAGATGGAATTTCATCTACGTCTTCCACACACTTG 600
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CTTTTCCTCACCACCCCGGATGGAGAAGATGGAATTTCATCTACGTCTTCCACACACTTG 600

Qy      601 GTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACAGCCAATG 660
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACAGCCAATG 660

Qy      661 TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG 720
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Db      661 TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG 720

Qy      721 TTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTGA 780
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Db      721 TTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTGA 780

Qy      781 CTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCC-CAAAGATCTCCCCA 839
                 ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
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Qy      840 TTATGTTTGATGTCCTGATTCATGATCCTAGCCACTTCCTCAATTATTCTACCATTAACT 899
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Qy      900 ACAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGTGAATC 959
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Db      901 ACAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGTGAATC 960

Qy      960 ACACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCAG 1019
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Qy     1020 GACCTTGTCCGCCACCGCCACCACCACCCAGACCTTCAAAACCCACCCCTTCTTTAGGAC 1079
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Qy   1080 CTGCTGGTGACAACCCCCTGGAGCTGAGTAGGATTCCTGATGAAAACTGCCAGATTAACA 1139
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Qy   1140 GATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATCA 1199
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Qy   1200 TCCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTG 1259
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Db   1201 TCCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTG 1260

Qy   1260 TCGTGACCTGCCAAGGGAGCATTCCCACGGAGGTCTGTACCATCATTTCTGACCCCACCT 1319
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Qy   1320 GCGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTGA 1379
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Qy   1380 CTGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCCTGGGGGATG 1439
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Qy   1440 ACACAAGCCTGGCTCTCACGAGCACCCTGATTTCTGTTCCTGACAGAGACCCAGCCTCGC 1499
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Qy   1500 CTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACTG 1559
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Qy   1560 TGATCTCCCTCTTGGTGTACAAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCTG 1619
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Qy   1680 TCCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTT 1739
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Qy   1740 AAATTTCGACCTTGTTTCTGAAGCTCACTTTTCAGTGCCATTGATGTGAGATGTGCTGGA 1799
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Qy   1800 GTGGCTATTAACCTTTTTTTCCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAA 1859
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Qy   1860 GTTGAATTTTTTATAGGTTAAATGTCATTTTAGAGATGGGGAGAGGGATTATACTGCAGG 1919
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Qy   1920 CAGCTTCAGCCATGTTGTGAAACTGATAAAAGCAACTTAGCAAGGCTTCTTTTCATTATT 1979
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Qy   1980 TTTTATGTTTCACTTATAAAGTCTTAGGTAACTAGTAGGATAGAAACACTGTGTCCCGAG 2039
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Qy   2040 AGTAAGGAGAGAAGCTACTATTGATTAGAGCCTAACCCAGGTTAACTGCAAGAAGAGGCG 2099
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Qy   2100 GGATACTTTCAGCTTTCCATGTAACTGTATGCATAAAGCCAATGTAGTCCAGTTTCTAAG 2159
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Qy   2160 ATCATGTTCCAAGCTAACTGAATCCCACTTCAATACACACTCATGAACTCCTGATGGAAC 2219
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Qy   2220 AATAACAGGCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGACTCAGAAAAAATACTA 2279
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Qy   2520 GATCAGTAAGGATTTCCCCTCTGTTTGGAACTAAAACCATTTACTATATGTTAGACAAGA 2579
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Qy   2580 CATTTTTTTTTTTCCTTCCTGAAAAAAAAATGAGGGAAGAGACAAAAAAAAAAAAAAAAA 2639
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Db   2581 CATTTTTTTTTTTCCTTCCTGAAAAAAAAATGAGGGAAGAGACAAAAAAAAAAAAAAAAA 2640

Qy   2640 AAAAAAAAAAAAAAAAAAAAA 2661
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Db   2641 AAAAAAAAAAAAAAAAAAAAA 2662


RESULT 2
AR018808
LOCUS       AR018808                 2669 bp    DNA     linear   PAT 05-DEC-1998
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DEFINITION   Sequence 91 from patent US 5783182.
ACCESSION   AR018808
VERSION   AR018808.1 GI:3973922
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
              Unclassified.
REFERENCE   1 (bases 1 to 2669)
  AUTHORS   Thompson,T.C.
  TITLE   Method for identifying metastatic sequences
  JOURNAL   Patent: US 5783182-A 91 21-JUL-1998;
FEATURES   Location/Qualifiers
     source   1. .2669
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

   Query Match   95.7%;   Score 2547.8; DB 6;   Length 2669;
   Best Local Similarity   99.2%;   Pred. No. 0;
   Matches 2591; Conservative   0; Mismatches   17; Indels   3; Gaps   3;

Qy   28 AACCTTGGTGCCTGCGTCCGTGAGAATTCAGCATGGAATGTCTCTACTATTTCCTGGGAT 87
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Db   60 ACCTTGAGTGCCTGCGTCCGTGAGAATTCAGCATGGAATGTCTCTACTATTTCCTGGGAT 119

Qy   88 TTCTGCTCCTGGCTGCAAGATTGCCACTTGATGCCGCCAAACGATTTCATGATGTGCTGG 147
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Db   120 TTCTGCTCCTGGCTGCAAGATTGCCACTTGATGCCGCCAAACGATTTCATGATGTGCTGG 179

Qy   148 GCAATGAAAGACCTTCTGCTTACATGAGGGAGCACAATCAATTAAATGGCTGGTCTTCTG 207
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Db   180 GCAATGAAAGACCTTCTGCTTACATGAGGGAGCACAATCAATTAAATGGCTGGTCTTCTG 239

Qy   208 ATGAAAATGACTGGAATGAAAAACTCTACCCAGTGTGGAAGCGGGGAGACATGAGGTGGA 267
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Qy   268 AAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCCCTCG 327
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Db   300 AAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCCCTCG 359

Qy   328 TGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGGAAGATG 387
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360 TGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGGAAGATG 419

Qy   388 CCAATGGCAACATAGTCTATGAGAAGAACTGCAGAAATGAGGCTGGTTTATCTGCTGATC 447
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420 CCAATGGCAACATAGTCTATGAGAAGAACTGCAGAAATGAGGCTGGTTTATCTGCTGATC 479

Qy   448 CATATGTTTACAACTGGACAGCATGGTCAGAGGACAGTGACGGGGAAAATGGCACCGGCC 507
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   480 CATATGTTTACAACTGGACAGCATGGTCAGAGGACAGTGACGGGGAAAATGGCACCGGCC 539

Qy   508 AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCCGGATGGAGAA 567
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   540 AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCCGGATGGAGAA 599

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Qy    568 GATGGAATTTCATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGAT 627
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Db    600 GATGGAATTTCATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGAT 659

Qy    628 GTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG 687
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Db    660 GTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG 719

Qy    688 TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGT 747
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGT 779

Qy    748 ACGTGGTAACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT 807
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 ACGTGGTAACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT 839

Qy    808 CATCCGACGAAACCTTCC-CAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC 866
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    840 CATCCGACGAAACCTTCCTCAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC 899

Qy    867 CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTG 926
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    900 CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTG 959

Qy    927 GCCTGTTTGTTTCCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGAACCTTCA 986
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Qy    987 GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCCACCGCCACCACCAC 1046
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Qy   1047 CCAGACCTTCAAAACCCACCCCTTCTTTAGGACCTGCTGGTGACAACCCCCTGGAGCTGA 1106
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 CCAGACCTTCAAAACCCACCCCTTCTTTAGGACCTGCTGGTGACAACCCCCTGGAGCTGA 1139

Qy   1107 GTAGGATTCCTGATGAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCA 1166
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 GTAGGATTCCTGATGAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCA 1199

Qy   1167 CAATTGTAGAGGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCCTGATGCCGG 1226
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 CAATTGTAGAGGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCCTGATGCCGG 1259

Qy   1227 TGCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCCA 1286
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 TGCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCCA 1319

Qy   1287 CGGAGGTCTGTACCATCATTTCTGACCCCACCTGCGAGATCACCCAGAACACAGTCTGCA 1346
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 CGGAGGTCTGTACCATCATTTCTGACCCCACCTGCGAGATCACCCAGAACACAGTCTGCA 1379

Qy   1347 GCCCTGTGGATGTGGATGAGATGTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTG 1406
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380 GCCCTGTGGATGTGGATGAGATGTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTG 1439

Qy   1407 GGACGTACTGTGTGAACCTCACCCTGGGGGATGACACAAGCCTGGCTCTCACGAGCACCC 1466
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        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1440 GGACGTACTGTGTGAACCTCACCCTGGGGGATGACACAAGCCTGGCTCTCACGAGCACCC 1499

Qy   1467 TGATTTCTGTTCCTGACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGA 1526
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Db   1500 TGATTTCTGTTCCTGACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGA 1559

Qy   1527 TCTCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTGGTGTACAAAAAAC 1586
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Db   1560 TCTCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTGGTGTACAAAAAAC 1619

Qy   1587 ACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGTGGTCAGAAGCAAAGGCCTGA 1646
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Qy   1647 GTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTTCCCGGGAAACCAGGAAAAGGATCCGC 1706
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Db   1740 TACTCAAAAACCAAGAATTTAAAGGAGTTTCTTAAATTTCGACCTTGTTTCTGAAGCTCA 1799

Qy   1767 CTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTGGCTATTAACCTTTTTTTCCTAAAG 1826
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Qy   1827 ATTATTGTTAAATAGATATTGTGGTTTGGGGAAGTTGAATTTTTTATAGGTTAAATGTCA 1886
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Db   1860 ATTATTGTTAAATAGATATTGTGGTTTGGGGAAGTTGAATTTTTTATAGGTTAAATGTCA 1919

Qy   1887 TTTTAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTCAGCCATGTTGTGAAACTGAT 1946
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1920 TTTTAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTCAGCCATGTTGTGAAACTGAT 1979

Qy   1947 AAAAGCAACTTAGCAAGGCTTCTTTTCATTATTTTTTATGTTTCACTTATAAAGTCTTAG 2006
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1980 AAAAGCAACTTAGCAAGGCTTCTTTTCATTATTTTTTATGTTTCACTTATAAAGTCTTAG 2039

Qy   2007 GTAACTAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAGAAGCTACTATTGATTA 2066
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Db   2040 GTAACTAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAGAAGCTACTATTGATTA 2099

Qy   2067 GAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGGGATACTTTCAGCTTTCCATGTAACTG 2126
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Qy   2127 TATGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCA 2186
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Db   2160 TATGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCA 2219

Qy   2187 CTTCAATACACACTCATGAACTCCTGATGGAACAATAACAGGCCCAAGCCTGTGGTATGA 2246
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Qy   2247 TGTGCACACTTGCTAGACTCAGAAAAAATACTACTCTCATAAATGGGTGGGAGTATTTTG 2306
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db      2280 TGTGCACACTTGCTAGACTCAGAAAAAATACTACTCTCATAAATGGGTGGGAGTATTTTG 2339

Qy      2307 GTGACAACCTACTTTGCTTGGCTGAGTGAAGGAATGATATTCATATATTCATTTATTCCA 2366
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Db      2340 GTGACAACCTACTTTGCTTGGCTGAGTGAAGGAATGATATTCATATATTCATTTATTCCA 2399

Qy      2367 TGGACATTTAGTTAGTGCTTTTTATATACCAGGCATGATGCTGAGTGACACTCTTGTGTA 2426
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      2427 TATTTCCAAATTTTTGTATAGTCGCTGCACATATTTGAAATCAAAATATTAAGACTTTCC 2486
             |||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
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Qy      2487 AAAAATTTGGTCCCTGGTTTTTCATGGCAACTTGATCAGTAAGGATTTCCCCTCTGTTTG 2546
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Db      2519 AAAGATGAGGTCCCTGGTTTTTCATGGCAACTTGATCAGTAAGGATTTCACCTCTGTTTG 2578

Qy      2547 GAACTAAAACCATTTACTATATGTTAGACAAGACATTTTTTTTTTTCCTTCCTGAAAAA 2606
             |||||||||||| |||||||||||||| |||||| |||||| | |||||||||||||||
Db      2579 TAACTAAAACCATCTACTATATGTTAGACATGACATTCTTTTTCTCTCCTTCCTGAAAAA 2638

Qy      2607 -AAAATGAGGGAAGAGACAAAAAAAAAAAAA 2636
              ||| || ||||||||||||||||||||||
Db      2639 TAAAGTGTGGGAAGAGACAAAAAAAAAAAAA 2669
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 21, 2005, 08:39:53 ; Search time 1308 Seconds
                                              (without alignments)
                                              12043.143 Million cell updates/sec

Title: US-10-039-272-1
Perfect score: 2661
Sequence: 1 cggcacgagggcccagagga.........aaaaaaaaaaaaaaaaaaaa 2661

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
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 3:  geneseqn2000s:*
 4:  geneseqn2001as:*
 5:  geneseqn2001bs:*
 6:  geneseqn2002as:*
 7:  geneseqn2002bs:*
 8:  geneseqn2003as:*
 9:  geneseqn2003bs:*
10:  geneseqn2003cs:*
11:  geneseqn2003ds:*
12:  geneseqn2004as:*
13:  geneseqn2004bs:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2661	100.0	2661	6	ABQ78551	Abq78551 Nucleotid
2	2571.2	96.6	2845	12	ADQ22838	Adq22838 Human sof
3	2559.2	96.2	2952	11	ACN89693	Acn89693 Breast ca
4	2547.8	95.7	2669	2	AAT69328	Aat69328 Murine me
5	2547.8	95.7	2669	2	AAT69318	Aat69318 Murine me
6	2547.8	95.7	2669	3	AAC55715	Aac55715 Human NMB
7	2547.8	95.7	2669	6	ABQ88185	Abq88185 Human ost
8	2547.8	95.7	2669	8	ABX76321	Abx76321 Lung canc
9	2547.8	95.7	2669	10	ADL14996	Adl14996 Human NMB
10	2547.8	95.7	2669	11	ADN39723	Adn39723 Cancer/an
11	2547.8	95.7	2669	12	ADJ75111	Adj75111 Marker ge
12	2547.8	95.7	2669	12	ADQ18309	Adq18309 Human sof
13	2547.8	95.7	2669	13	ADR24918	Adr24918 Breast ca
14	2547.8	95.7	2669	13	ADP23126	Adp23126 PRO polyp
15	2547.8	95.7	2669	13	ADR66172	Adr66172 Human pro
16	2547.8	95.7	2669	13	ADR66150	Adr66150 Human pro
17	2531.6	95.1	2666	10	ADJ56363	Adj56363 Human cDN
18	2505.6	94.2	2728	10	ADD78274	Add78274 Human CGD
19	2485	93.4	2683	6	ABK33556	Abk33556 cDNA enco
20	2485	93.4	2683	8	ACA68517	Aca68517 Novel hum
21	2485	93.4	2683	9	ABT44246	Abt44246 Human PRO
22	2485	93.4	2683	9	ABT44529	Abt44529 Human PRO
23	2485	93.4	2683	9	ACD82196	Acd82196 Human sec
24	2485	93.4	2683	9	ABT43902	Abt43902 Human mem
25	2485	93.4	2683	9	ADB83531	Adb83531 Novel hum
26	2485	93.4	2683	9	ADB80637	Adb80637 Novel hum
27	2485	93.4	2683	9	ADB73178	Adb73178 Novel hum
28	2485	93.4	2683	9	ADB78260	Adb78260 Novel hum
29	2485	93.4	2683	10	ADB84908	Adb84908 Human PRO
30	2485	93.4	2683	10	ADB78014	Adb78014 Novel hum
31	2485	93.4	2683	10	ADB87080	Adb87080 Human PRO
32	2485	93.4	2683	10	ADB84662	Adb84662 Human PRO
33	2485	93.4	2683	10	ADB83777	Adb83777 Novel hum
34	2485	93.4	2683	10	ADB72932	Adb72932 Novel hum
35	2485	93.4	2683	10	ADC36770	Adc36770 Human PRO
36	2485	93.4	2683	10	ADC21760	Adc21760 Human PRO

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37    2485   93.4   2683   10   ADC49791          Adc49791 Novel hum
38    2485   93.4   2683   10   ADC48990          Adc48990 Novel hum
39    2485   93.4   2683   10   ADC49507          Adc49507 Novel hum
40    2485   93.4   2683   10   ADC47368          Adc47368 Novel hum
41    2485   93.4   2683   10   ADC47113          Adc47113 Novel hum
42    2485   93.4   2683   10   ADC77988          Adc77988 Novel hum
43    2485   93.4   2683   10   ADD06223          Add06223 Novel hum
44    2485   93.4   2683   10   ADC77742          Adc77742 Novel hum
45    2485   93.4   2683   10   ADD50705          Add50705 Novel hum
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ALIGNMENTS

RESULT 1
ABQ78551
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ID    ABQ78551 standard; DNA; 2661 BP.
XX
AC    ABQ78551;
XX
DT    25-NOV-2002  (first entry)
XX
DE    Nucleotide sequence of human HGFIN.
XX
KW    Human; cell differentiation; white blood cell; bone marrow cell;
KW    haematopoietic growth factor inducible neurokin-1; HGFIN;
KW    progenitor proliferation; acute myeloid leukemia; non-Hodgkin's disease;
KW    acute lymphocytic leukemia; chronic myeloid leukemia;
KW    chronic lymphocytic leukemia; Hodgkin's disease; gene; ss.
XX
OS    Homo sapiens.
XX
FH    Key           Location/Qualifiers
FT    CDS           60. .1741
FT                  /*tag=  a
FT                  /product= "HGFIN"
FT                  /transl_except= (825. .826,aa:Leu)
XX
PN    WO200262947-A2.
XX
PD    15-AUG-2002.
XX
PF    20-OCT-2001; 2001WO-US050204.
XX
PR    20-OCT-2000; 2000US-0241881P.
XX
PA    (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI    Pranela R;
XX
DR    WPI; 2002-657531/70.
DR    P-PSDB; ABB78200.
XX
PT    Hematopoietic growth factor inducible neurokin-1 type polypeptide and
PT    polynucleotide for treating a disease associated with abnormal bone
PT    marrow cell differentiation or proliferation, e.g. leukemia.
XX
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PS   Claim 2; Page 121-123; 125pp; English.
XX
CC   The present sequence encodes human haematopoietic growth factor inducible
CC   neurokin-1 type (HGFIN) polypeptide. HGFIN induces white blood cell
CC   differentiation and inhibits progenitor proliferation. HGFIN polypeptides
CC   and polynucleotides are useful for treating a disease associated with
CC   abnormal bone marrow cell differentiation or proliferation, especially
CC   acute myeloid leukemia, acute lymphocytic leukemia, chronic myeloid
CC   leukemia, chronic lymphocytic leukemia, Hodgkin's and non-Hodgkin's
CC   disease
XX
SQ   Sequence 2661 BP; 772 A; 586 C; 587 G; 716 T; 0 U; 0 Other;

      Query Match   100.0%;   Score 2661;   DB 6;   Length 2661;
      Best Local Similarity   100.0%;   Pred. No. 0;
      Matches 2661; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CGGCACGAGGGCCCAGAGGAATAAGTTAACCTTGGTGCCTGCGTCCGTGAGAATTCAGCA 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CGGCACGAGGGCCCAGAGGAATAAGTTAACCTTGGTGCCTGCGTCCGTGAGAATTCAGCA 60

Qy   61 TGGAATGTCTCTACTATTTCCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGATG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGGAATGTCTCTACTATTTCCTGGGATTTCTGCTCCTGGCTGCAAGATTGCCACTTGATG 120

Qy   121 CCGCCAAACGATTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAGC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCGCCAAACGATTTCATGATGTGCTGGGCAATGAAAGACCTTCTGCTTACATGAGGGAGC 180

Qy   181 ACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAAACTCTACCCAG 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGAAAAACTCTACCCAG 240

Qy   241 TGTGGAAGCGGGGAGACATGAGGTGGAAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TGTGGAAGCGGGGAGACATGAGGTGGAAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGG 300

Qy   301 TCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTGA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTGA 360

Qy   361 TATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGCA 420
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Db   361 TATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGCA 420

Qy   421 GAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACTGGACAGCATGGTCAGAGG 480
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Db   421 GAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACTGGACAGCATGGTCAGAGG 480

Qy   481 ACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAAC 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAAC 540

Qy   541 CTTTTCCTCACCACCCCGGATGGAGAAGATGGAATTTCATCTACGTCTTCCACACACTTG 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    601 GTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACAGCCAATG 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACAGCCAATG 660

Qy    661 TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG 720

Qy    721 TTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTGA 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTGA 780

Qy    781 CTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCCAAAGATCTCCCCAT 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCCAAAGATCTCCCCAT 840

Qy    841 TATGTTTGATGTCCTGATTCATGATCCTAGCCACTTCCTCAATTATTCTACCATTAACTA 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TATGTTTGATGTCCTGATTCATGATCCTAGCCACTTCCTCAATTATTCTACCATTAACTA 900

Qy    901 CAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGTGAATCA 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGTGAATCA 960

Qy    961 CACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCAGG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CACGTATGTGCTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCAGG 1020

Qy   1021 ACCTTGTCCGCCACCGCCACCACCACCCAGACCTTCAAAACCCACCCCTTCTTTAGGACC 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ACCTTGTCCGCCACCGCCACCACCACCCAGACCTTCAAAACCCACCCCTTCTTTAGGACC 1080

Qy   1081 TGCTGGTGACAACCCCCTGGAGCTGAGTAGGATTCCTGATGAAAACTGCCAGATTAACAG 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGCTGGTGACAACCCCCTGGAGCTGAGTAGGATTCCTGATGAAAACTGCCAGATTAACAG 1140

Qy   1141 ATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATCAT 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATCAT 1200

Qy   1201 CCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTGT 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTGT 1260

Qy   1261 CGTGACCTGCCAAGGGAGCATTCCCACGGAGGTCTGTACCATCATTTCTGACCCCACCTG 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 CGTGACCTGCCAAGGGAGCATTCCCACGGAGGTCTGTACCATCATTTCTGACCCCACCTG 1320

Qy   1321 CGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTGAC 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTGAC 1380

Qy   1381 TGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCCTGGGGGATGA 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCCTGGGGGATGA 1440

Qy   1441 CACAAGCCTGGCTCTCACGAGCACCCTGATTTCTGTTCCTGACAGAGACCCAGCCTCGCC 1500
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Db      1441  CACAAGCCTGGCTCTCACGAGCACCCTGATTTCTGTTCCTGACAGAGACCCAGCCTCGCC  1500

Qy      1501  TTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACTGT  1560
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1501  TTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACTGT  1560

Qy      1561  GATCTCCCTCTTGGTGTACAAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCTGG  1620
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1561  GATCTCCCTCTTGGTGTACAAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCTGG  1620

Qy      1621  GAATGTGGTCAGAAGCAAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTT  1680
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1621  GAATGTGGTCAGAAGCAAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTT  1680

Qy      1681  CCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTTA  1740
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1681  CCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTTA  1740

Qy      1741  AATTTCGACCTTGTTTCTGAAGCTCACTTTTCAGTGCCATTGATGTGAGATGTGCTGGAG  1800
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1741  AATTTCGACCTTGTTTCTGAAGCTCACTTTTCAGTGCCATTGATGTGAGATGTGCTGGAG  1800

Qy      1801  TGGCTATTAACCTTTTTTTCCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAAG  1860
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1801  TGGCTATTAACCTTTTTTTCCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAAG  1860

Qy      1861  TTGAATTTTTTATAGGTTAAATGTCATTTTAGAGATGGGGAGAGGGATTATACTGCAGGC  1920
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1861  TTGAATTTTTTATAGGTTAAATGTCATTTTAGAGATGGGGAGAGGGATTATACTGCAGGC  1920

Qy      1921  AGCTTCAGCCATGTTGTGAAACTGATAAAAGCAACTTAGCAAGGCTTCTTTTCATTATTT  1980
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1921  AGCTTCAGCCATGTTGTGAAACTGATAAAAGCAACTTAGCAAGGCTTCTTTTCATTATTT  1980

Qy      1981  TTTATGTTTCACTTATAAAGTCTTAGGTAACTAGTAGGATAGAAACACTGTGTCCCGAGA  2040
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1981  TTTATGTTTCACTTATAAAGTCTTAGGTAACTAGTAGGATAGAAACACTGTGTCCCGAGA  2040

Qy      2041  GTAAGGAGAGAAGCTACTATTGATTAGAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGG  2100
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2041  GTAAGGAGAGAAGCTACTATTGATTAGAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGG  2100

Qy      2101  GATACTTTCAGCTTTCCATGTAACTGTATGCATAAAGCCAATGTAGTCCAGTTTCTAAGA  2160
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2101  GATACTTTCAGCTTTCCATGTAACTGTATGCATAAAGCCAATGTAGTCCAGTTTCTAAGA  2160

Qy      2161  TCATGTTCCAAGCTAACTGAATCCCACTTCAATACACACTCATGAACTCCTGATGGAACA  2220
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2161  TCATGTTCCAAGCTAACTGAATCCCACTTCAATACACACTCATGAACTCCTGATGGAACA  2220

Qy      2221  ATAACAGGCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGACTCAGAAAAAATACTAC  2280
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2221  ATAACAGGCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGACTCAGAAAAAATACTAC  2280

Qy      2281  TCTCATAAATGGGTGGGAGTATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGAA  2340
                    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db    2281 TCTCATAAATGGGTGGGAGTATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGAA 2340

Qy    2341 TGATATTCATATATTCATTTATTCCATGGACATTTAGTTAGTGCTTTTTATATACCAGGC 2400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 TGATATTCATATATTCATTTATTCCATGGACATTTAGTTAGTGCTTTTTATATACCAGGC 2400

Qy    2401 ATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTTGTATAGTCGCTGCACATAT 2460
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 ATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTTGTATAGTCGCTGCACATAT 2460

Qy    2461 TTGAAATCAAAATATTAAGACTTTCCAAAAATTTGGTCCCTGGTTTTTCATGGCAACTTG 2520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461 TTGAAATCAAAATATTAAGACTTTCCAAAAATTTGGTCCCTGGTTTTTCATGGCAACTTG 2520

Qy    2521 ATCAGTAAGGATTTCCCCTCTGTTTGGAACTAAAACCATTTACTATATGTTAGACAAGAC 2580
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521 ATCAGTAAGGATTTCCCCTCTGTTTGGAACTAAAACCATTTACTATATGTTAGACAAGAC 2580

Qy    2581 ATTTTTTTTTTTCCTTCCTGAAAAAAAAATGAGGGAAGAGACAAAAAAAAAAAAAAAAAA 2640
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581 ATTTTTTTTTTTCCTTCCTGAAAAAAAAATGAGGGAAGAGACAAAAAAAAAAAAAAAAAA 2640

Qy    2641 AAAAAAAAAAAAAAAAAAAAA 2661
           |||||||||||||||||||||
Db    2641 AAAAAAAAAAAAAAAAAAAAA 2661


RESULT 2
ADQ22838
ID    ADQ22838 standard; DNA; 2845 BP.
XX
AC    ADQ22838;
XX
DT    26-AUG-2004  (first entry)
XX
DE    Human soft tissue sarcoma-upregulated DNA - SEQ ID 5658.
XX
KW    soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW    ds.
XX
OS    Homo sapiens.
XX
PN    WO2004048938-A2.
XX
PD    10-JUN-2004.
XX
PF    26-NOV-2003; 2003WO-US038193.
XX
PR    26-NOV-2002; 2002US-0429739P.
XX
PA    (PROT-) PROTEIN DESIGN LABS INC.
XX
PI    Aziz N,  Ginsburg WM,  Zlotnik A;
XX
DR    WPI; 2004-441208/41.
XX
PT    Early detection of soft tissue sarcoma comprises determining expression
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PT    of a gene in a first soft tissue sample and a normal soft tissue sample
PT    and comparing the gene expression, also useful in treating soft tissue
PT    sarcoma.
XX
PS    Example 2; SEQ ID NO 5658; 210pp; English.
XX
CC    The invention relates to a novel method for detecting soft tissue sarcoma
CC    which comprises obtaining a first soft tissue sample from an individual
CC    and a normal soft tissue sample from the same or different individual,
CC    determining the expression of a gene in both samples and comparing the
CC    expression of the gene in both soft tissue samples, where a higher level
CC    of protein expression in the first soft tissue sample indicates the
CC    presence of soft tissue sarcoma. The method of the invention has
CC    cytostatic applications and may be useful for detecting soft tissue
CC    sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC    acid sequences may be useful in diagnostic and screening applications.
CC    The current sequence is that of a human soft tissue sarcoma-upregulated
CC    DNA of the invention. The current sequence is not shown within the
CC    specification per se but was submitted in CD format by the inventor.
XX
SQ    Sequence 2845 BP; 873 A; 617 C; 614 G; 741 T; 0 U; 0 Other;

   Query Match              96.6%;   Score 2571.2;   DB 12;   Length 2845;
   Best Local Similarity    99.2%;   Pred. No. 0;
   Matches 2615;  Conservative    0;  Mismatches   18;  Indels    3;  Gaps    3;

Qy        28 AACCTTGGTGCCTGCGTCCGTGAGAATTCAGCATGGAATGTCTCTACTATTTCCTGGGAT 87
              I  I  I     IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       140 ACCTTGAGTGCCTGCGTCCGTGAGAATTCAGCATGGAATGTCTCTACTATTTCCTGGGAT 199

Qy        88 TTCTGCTCCTGGCTGCAAGATTGCCACTTGATGCCGCCAAACGATTTCATGATGTGCTGG 147
              IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       200 TTCTGCTCCTGGCTGCAAGATTGCCACTTGATGCCGCCAAACGATTTCATGATGTGCTGG 259

Qy       148 GCAATGAAAGACCTTCTGCTTACATGAGGGAGCACAATCAATTAAATGGCTGGTCTTCTG 207
              IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       260 GCAATGAAAGACCTTCTGCTTACATGAGGGAGCACAATCAATTAAATGGCTGGTCTTCTG 319

Qy       208 ATGAAAATGACTGGAATGAAAAACTCTACCCAGTGTGGAAGCGGGGAGACATGAGGTGGA 267
              IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       320 ATGAAAATGACTGGAATGAAAAACTCTACCCAGTGTGGAAGCGGGGAGACATGAGGTGGA 379

Qy       268 AAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCCCTCG 327
              IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       380 AAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCCCTCG 439

Qy       328 TGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGGAAGATG 387
              IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       440 TGGGCTCAAATATAACATTTGCGGTGAACCTGATATTCCCTAGATGCCAAAAGGAAGATG 499

Qy       388 CCAATGGCAACATAGTCTATGAGAAGAACTGCAGAAATGAGGCTGGTTTATCTGCTGATC 447
              IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       500 CCAATGGCAACATAGTCTATGAGAAGAACTGCAGAAATGAGGCTGGTTTATCTGCTGATC 559

Qy       448 CATATGTTTACAACTGGACAGCATGGTCAGAGGACAGTGACGGGGAAAATGGCACCGGCC 507
              IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       560 CATATGTTTACAACTGGACAGCATGGTCAGAGGACAGTGACGGGGAAAATGGCACCGGCC 619
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Qy    508 AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCCGGATGGAGAA 567
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    620 AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCCGGATGGAGAA 679

Qy    568 GATGGAATTTCATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGAT 627
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    680 GATGGAATTTCATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGAT 739

Qy    628 GTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG 687
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    740 GTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG 799

Qy    688 TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGT 747
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    800 TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGT 859

Qy    748 ACGTGGTAACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT 807
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    860 ACGTGGTAACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT 919

Qy    808 CATCCGACGAAACCTTCC-CAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC 866
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    920 CATCCGACGAAACCTTCCTCAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC 979

Qy    867 CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTG 926
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    980 CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTG 1039

Qy    927 GCCTGTTTGTTTCCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGAACCTTCA 986
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1040 GCCTGTTTGTTTCCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGAACCTTCA 1099

Qy    987 GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCCACCGCCACCACCAC 1046
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1100 GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCCACCGCCACCACCAC 1159

Qy   1047 CCAGACCTTCAAAACCCACCCCTTCTTTAGGACCTGCTGGTGACAACCCCCTGGAGCTGA 1106
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1160 CCAGACCTTCAAAACCCACCCCTTCTTTAGGACCTGCTGGTGACAACCCCCTGGAGCTGA 1219

Qy   1107 GTAGGATTCCTGATGAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCA 1166
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1220 GTAGGATTCCTGATGAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCA 1279

Qy   1167 CAATTGTAGAGGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCCTGATGCCGG 1226
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1280 CAATTGTAGAGGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCCTGATGCCGG 1339

Qy   1227 TGCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCCA 1286
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1340 TGCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCCA 1399

Qy   1287 CGGAGGTCTGTACCATCATTTCTGACCCCACCTGCGAGATCACCCAGAACACAGTCTGCA 1346
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1400 CGGAGGTCTGTACCATCATTTCTGACCCCACCTGCGAGATCACCCAGAACACAGTCTGCA 1459
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Qy    1347 GCCCTGTGGATGTGGATGAGATGTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTG 1406
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1460 GCCCTGTGGATGTGGATGAGATGTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTG 1519

Qy    1407 GGACGTACTGTGTGAACCTCACCCTGGGGGATGACACAAGCCTGGCTCTCACGAGCACCC 1466
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1520 GGACGTACTGTGTGAACCTCACCCTGGGGGATGACACAAGCCTGGCTCTCACGAGCACCC 1579

Qy    1467 TGATTTCTGTTCCTGACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGA 1526
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1580 TGATTTCTGTTCCTGACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGA 1639

Qy    1527 TCTCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTGGTGTACAAAAAAC 1586
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1640 TCTCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTGGTGTACAAAAAAC 1699

Qy    1587 ACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGTGGTCAGAAGCAAAGGCCTGA 1646
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1700 ACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGTGGTCAGAAGCAAAGGCCTGA 1759

Qy    1647 GTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTTCCCGGGAAACCAGGAAAAGGATCCGC 1706
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1760 GTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTTCCCGGGAAACCAGGAAAAGGATCCGC 1819

Qy    1707 TACTCAAAAACCAAGAATTTAAAGGAGTTTCTTAAATTTCGACCTTGTTTCTGAAGCTCA 1766
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1820 TACTCAAAAACCAAGAATTTAAAGGAGTTTCTTAAATTTCGACCTTGTTTCTGAAGCTCA 1879

Qy    1767 CTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTGGCTATTAACCTTTTTTTCCTAAAG 1826
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1880 CTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTGGCTATTAACCTTTTTTTCCTAAAG 1939

Qy    1827 ATTATTGTTAAATAGATATTGTGGTTTGGGGAAGTTGAATTTTTTATAGGTTAAATGTCA 1886
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1940 ATTATTGTTAAATAGATATTGTGGTTTGGGGAAGTTGAATTTTTTATAGGTTAAATGTCA 1999

Qy    1887 TTTTAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTCAGCCATGTTGTGAAACTGAT 1946
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2000 TTTTAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTCAGCCATGTTGTGAAACTGAT 2059

Qy    1947 AAAAGCAACTTAGCAAGGCTTCTTTTCATTATTTTTTATGTTTCACTTATAAAGTCTTAG 2006
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2060 AAAAGCAACTTAGCAAGGCTTCTTTTCATTATTTTTTATGTTTCACTTATAAAGTCTTAG 2119

Qy    2007 GTAACTAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAGAAGCTACTATTGATTA 2066
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2120 GTAACTAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAGAAGCTACTATTGATTA 2179

Qy    2067 GAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGGGATACTTTCAGCTTTCCATGTAACTG 2126
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2180 GAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGGGATACTTTCAGCTTTCCATGTAACTG 2239

Qy    2127 TATGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCA 2186
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2005, 10:32:04 ; Search time 458 Seconds
                                        (without alignments)
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Perfect score: 2661
Sequence: 1 cggcacgagggcccagagga.........aaaaaaaaaaaaaaaaaaaa 2661

Scoring table: IDENTITY_NUC
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%

Listing first 45 summaries

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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES

		% Query				
Result						
No.	Score	Match	Length	DB	ID	Description
1	2547.8	95.7	2669	1	US-09-985-799-91	Sequence 91, Appl
2	2547.8	95.7	2669	1	US-09-985-799-101	Sequence 101, App
3	2547.8	95.7	2669	1	US-09-977-371-91	Sequence 91, Appl
4	2547.8	95.7	2669	1	US-09-977-371-101	Sequence 101, App
5	2547.8	95.7	2669	1	US-08-594-031-91	Sequence 91, Appl
6	2547.8	95.7	2669	1	US-08-594-031-101	Sequence 101, App
7	1664.6	62.6	1683	4	US-09-943-075A-8	Sequence 8, Appli
8	1051.2	39.5	2303	4	US-09-197-970B-4	Sequence 4, Appli
9	1047.8	39.4	2213	3	US-09-383-586-27	Sequence 27, Appl
10	1047.8	39.4	2213	4	US-09-823-038A-27	Sequence 27, Appl
11	1046.4	39.3	2320	4	US-09-943-075A-1	Sequence 1, Appli
12	1010.2	38.0	1725	4	US-09-943-075A-7	Sequence 7, Appli
13	545.6	20.5	619	3	US-09-123-912-105	Sequence 105, App
14	545.6	20.5	619	3	US-09-643-597-105	Sequence 105, App
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38	493	18.5	494	4	US-09-551-621-449	Sequence 449, App

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40    480.8    18.1    698    3    US-09-123-912-5         Sequence 5, Appli
41    480.8    18.1    698    3    US-09-643-597-5         Sequence 5, Appli
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ALIGNMENTS

RESULT 1
US-09-985-799-91
; Sequence 91, Application US/09985799
; Patent No. RE38392
;   GENERAL INFORMATION:
;   APPLICANT: THOMPSON, Timothy C.
;   TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
;   NUMBER OF SEQUENCES: 175
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BAKER & BOTTS, L.L.P.
;   STREET: 1299 Pennsylvania Avenue, N.W.
;   CITY: Washington
;   STATE: DC
;   COUNTRY: USA
;   ZIP: 20004-2400
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/985,799
;   FILING DATE: 06-No. RE38392-2001
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/594,031
;   FILING DATE: 30-JAN-1996
;   APPLICATION NUMBER: 60/006,838
;   FILING DATE: 16-NOV-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Remenick, James
;   REGISTRATION NUMBER: 36,902
;   REFERENCE/DOCKET NUMBER: 0A146-0110
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-639-7700
;   TELEFAX: 202-639-7890
;   TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 91:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2669 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
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  Query Match              95.7%;   Score 2547.8;   DB 1;   Length 2669;
  Best Local Similarity    99.2%;   Pred. No. 0;
  Matches 2591;  Conservative    0;  Mismatches   17;  Indels   3;  Gaps    3;
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Qy      28 AACCTTGGTGCCTGCGTCCGTGAGAATTCAGCATGGAATGTCTCTACTATTTCCTGGGAT 87
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Qy     268 AAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGGTCCTGACCAGTGACTCACCAGCCCTCG 327
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Qy   2427  TATTTCCAAATTTTTGTATAGTCGCTGCACATATTTGAAATCAAAATATTAAGACTTTCC  2486
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Db      2639  TAAAGTGTGGGAAGAGACAAAAAAAAAAAAAA 2669




                        GenCore version 5.1.6
                 Copyright (c) 1993 - 2005  Compugen Ltd.



OM nucleic - nucleic search, using sw model

Run on:           February 21, 2005, 14:08:32 ; Search time 1392 Seconds
                                              (without alignments)
                                              11298.729 Million cell updates/sec


Title:            US-10-039-272-1
Perfect score:    2661
Sequence:         1 cggcacgagggcccagagga.........aaaaaaaaaaaaaaaaaaaaa 2661

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters:       10768316

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2661	100.0	2661	13	US-10-039-272-1	Sequence 1, Appli
2	2661	100.0	2661	17	US-10-463-106-1	Sequence 1, Appli
3	2571.2	96.6	2845	18	US-10-723-860-5658	Sequence 5658, Ap
4	2559.2	96.2	2952	14	US-10-198-846-10843	Sequence 10843, A
5	2547.8	95.7	2669	10	US-09-525-978B-82	Sequence 82, Appl
6	2547.8	95.7	2669	17	US-10-172-118-779	Sequence 779, App
7	2547.8	95.7	2669	17	US-10-295-027-1041	Sequence 1041, Ap
8	2547.8	95.7	2669	17	US-10-342-887-779	Sequence 779, App
9	2547.8	95.7	2669	18	US-10-450-826-92	Sequence 92, Appl
10	2547.8	95.7	2669	18	US-10-723-860-1127	Sequence 1127, Ap
11	2531.6	95.1	2666	15	US-10-084-817-169	Sequence 169, App
12	2485	93.4	2683	14	US-10-227-884-41	Sequence 41, Appl
13	2485	93.4	2683	14	US-10-230-163-41	Sequence 41, Appl
14	2485	93.4	2683	14	US-10-230-338-41	Sequence 41, Appl
15	2485	93.4	2683	14	US-10-218-631-41	Sequence 41, Appl
16	2485	93.4	2683	14	US-10-230-414-41	Sequence 41, Appl
17	2485	93.4	2683	14	US-10-232-224-41	Sequence 41, Appl
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44	2485	93.4	2683	14	US-10-227-880-41	Sequence 41, Appl
45	2485	93.4	2683	14	US-10-227-881-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-10-039-272-1
; Sequence 1, Application US/10039272
; Publication No. US20020168653A1
; GENERAL INFORMATION:
; APPLICANT: RAMESHWAR, Pranela
; . TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE NEUROKININ-TYPE
; FILE REFERENCE: 267/033 University of Medicine & Dentistry of New Jersey
; CURRENT APPLICATION NUMBER: US/10/039,272
; CURRENT FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/241,881
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2661
; .TYPE: DNA
; ORGANISM: Homo sapiens
US-10-039-272-1

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Qy    2641 AAAAAAAAAAAAAAAAAAAA 2661
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RESULT 2
US-10-463-106-1
; Sequence 1, Application US/10463106
; Publication No. US20030202938A1
; GENERAL INFORMATION:
; APPLICANT: RAMESHWAR, Pranela
; TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE NEUROKININ-1 GENE
; FILE REFERENCE: 267/033 University of Medicine & Dentistry of New Jersey
; CURRENT APPLICATION NUMBER: US/10/463,106
; CURRENT FILING DATE: 2003-06-17

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  Best Local Similarity    100.0%;  Pred. No. 0;
  Matches 2661; Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


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Qy        241 TGTGGAAGCGGGGAGACATGAGGTGGAAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGG 300
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Db        241 TGTGGAAGCGGGGAGACATGAGGTGGAAAAACTCCTGGAAGGGAGGCCGTGTGCAGGCGG 300

Qy        301 TCCTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCGGTGAACCTGA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 TATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGCA 420
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Db        361 TATTCCCTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAAGAACTGCA 420

Qy        421 GAAATGAGGCTGGTTTATCTGCTGATCCATATGTTTACAACTGGACAGCATGGTCAGAGG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        481 ACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAAC 540
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Db        481 ACAGTGACGGGGAAAATGGCACCGGCCAAAGCCATCATAACGTCTTCCCTGATGGGAAAC 540

Qy        541 CTTTTCCTCACCACCCCGGATGGAGAAGATGGAATTTCATCTACGTCTTCCACACACTTG 600
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Db        541 CTTTTCCTCACCACCCCGGATGGAGAAGATGGAATTTCATCTACGTCTTCCACACACTTG 600

Qy        601 GTCAGTATTTCCAGAAAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACAGCCAATG 660
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                  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        601    GTCAGTATTTCCAGAAATTGGGACGATGTTCAGTGAGAGTTTCTGTGAACACAGCCAATG    660

Qy        661    TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG    720
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Db        661    TGACACTTGGGCCTCAACTCATGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATG    720

Qy        721    TTCCCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTGA    780
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Qy        781    CTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCCAAAGATCTCCCCAT    840
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Db        781    CTATGTTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCCAAAGATCTCCCCAT    840

Qy        841    TATGTTTGATGTCCTGATTCATGATCCTAGCCACTTCCTCAATTATTCTACCATTAACTA    900
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Qy        901    CAAGTGGAGCTTCGGGGATAATACTGGCCTGTTTGTTTCCACCAATCATACTGTGAATCA    960
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Qy        1021   ACCTTGTCCGCCACCGCCACCACCACCCAGACCTTCAAAACCCACCCCTTCTTTAGGACC    1080
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Qy        1081   TGCTGGTGACAACCCCCTGGAGCTGAGTAGGATTCCTGATGAAAACTGCCAGATTAACAG    1140
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Qy        1141   ATATGGCCACTTTCAAGCCACCATCACAATTGTAGAGGGAATCTTAGAGGTTAACATCAT    1200
                  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Qy        1201   CCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTGT    1260
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Db        1201   CCAGATGACAGACGTCCTGATGCCGGTGCCATGGCCTGAAAGCTCCCTAATAGACTTTGT    1260

Qy        1261   CGTGACCTGCCAAGGGAGCATTCCCACGGAGGTCTGTACCATCATTTCTGACCCCACCTG    1320
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Db        1261   CGTGACCTGCCAAGGGAGCATTCCCACGGAGGTCTGTACCATCATTTCTGACCCCACCTG    1320

Qy        1321   CGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTGAC    1380
                  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        1321   CGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGATGTGTCTGCTGAC    1380

Qy        1381   TGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCCTGGGGGATGA    1440
                  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        1381   TGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCCTGGGGGATGA    1440

Qy        1441   CACAAGCCTGGCTCTCACGAGCACCCTGATTTCTGTTCCTGACAGAGACCCAGCCTCGCC    1500
                  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db   1441 CACAAGCCTGGCTCTCACGAGCACCCTGATTTCTGTTCCTGACAGAGACCCAGCCTCGCC 1500

Qy   1501 TTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACTGT 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGTCACTGT 1560

Qy   1561 GATCTCCCTCTTGGTGTACAAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCTGG 1620
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Db   1561 GATCTCCCTCTTGGTGTACAAAAAACACAAGGAATACAACCCAATAGAAAATAGTCCTGG 1620

Qy   1621 GAATGTGGTCAGAAGCAAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTT 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GAATGTGGTCAGAAGCAAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTT 1680

Qy   1681 CCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTTA 1740
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Db   1681 CCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTTA 1740

Qy   1741 AATTTCGACCTTGTTTCTGAAGCTCACTTTTCAGTGCCATTGATGTGAGATGTGCTGGAG 1800
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Qy   1801 TGGCTATTAACCTTTTTTTCCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAAG 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 TGGCTATTAACCTTTTTTTCCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAAG 1860

Qy   1861 TTGAATTTTTTATAGGTTAAATGTCATTTTAGAGATGGGGAGAGGGATTATACTGCAGGC 1920
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Db   1921 AGCTTCAGCCATGTTGTGAAACTGATAAAAGCAACTTAGCAAGGCTTCTTTTCATTATTT 1980

Qy   1981 TTTATGTTTCACTTATAAAGTCTTAGGTAACTAGTAGGATAGAAACACTGTGTCCCGAGA 2040
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Qy   2041 GTAAGGAGAGAAGCTACTATTGATTAGAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGG 2100
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Qy   2101 GATACTTTCAGCTTTCCATGTAACTGTATGCATAAAGCCAATGTAGTCCAGTTTCTAAGA 2160
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Qy   2161 TCATGTTCCAAGCTAACTGAATCCCACTTCAATACACACTCATGAACTCCTGATGGAACA 2220
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Qy   2221 ATAACAGGCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGACTCAGAAAAAATACTAC 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 ATAACAGGCCCAAGCCTGTGGTATGATGTGCACACTTGCTAGACTCAGAAAAAATACTAC 2280

Qy   2281 TCTCATAAATGGGTGGGAGTATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGAA 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TCTCATAAATGGGTGGGAGTATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGAA 2340
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Qy      2341 TGATATTCATATATTCATTTATTCCATGGACATTTAGTTAGTGCTTTTTATATACCAGGC 2400
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Qy      2401 ATGATGCTGAGTGACACTCTTGTGTATATTTCCAAATTTTTGTATAGTCGCTGCACATAT 2460
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Qy      2461 TTGAAATCAAAATATTAAGACTTTCCAAAAATTTGGTCCCTGGTTTTTCATGGCAACTTG 2520
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Qy      2641 AAAAAAAAAAAAAAAAAAAA 2661
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Db      2641 AAAAAAAAAAAAAAAAAAAA 2661
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2005, 10:29:04 ; Search time 7723 Seconds
                                        (without alignments)
                                        13115.243 Million cell updates/sec

Title: US-10-039-272-1
Perfect score: 2661
Sequence: 1 cggcacgagggcccagagga.........aaaaaaaaaaaaaaaaaaaa 2661

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est2:*

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                          3:  gb_htc:*
                          4:  gb_est3:*
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                          6:  gb_est5:*
                          7:  gb_est6:*
                          8:  gb_gss1:*
                          9:  gb_gss2:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
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<div align="center">SUMMARIES</div>

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2550	95.8	2636	3	BC025297	BC025297 Homo sapi
	2	1698	63.8	1757	3	CR620418	CR620418 full-leng
	3	1664.8	62.6	1695	3	CR625459	CR625459 full-leng
	4	1617	60.8	1726	3	CR626032	CR626032 full-leng
	5	1049.8	39.5	3615	3	AK044764	AK044764 Mus muscu
	6	1046.6	39.3	2265	3	AK076347	AK076347 Mus muscu
c	7	1017.4	38.2	1106	5	BX397314	BX397314 BX397314
c	8	1013.6	38.1	1050	5	BX379978	BX379978 BX379978
	9	943.8	35.5	2431	3	AK079220	AK079220 Mus muscu
c	10	932.6	35.0	971	5	BX423077	BX423077 BX423077
c	11	926.6	34.8	1015	5	BX458448	BX458448 BX458448
	12	918	34.5	1029	5	BX406949	BX406949 BX406949
	13	913.6	34.3	998	5	BX379979	BX379979 BX379979
	14	910.6	34.2	1063	5	BX336884	BX336884 BX336884
	15	906.4	34.1	1067	5	BX364871	BX364871 BX364871
	16	885.6	33.3	947	5	BX458449	BX458449 BX458449
	17	867.4	32.6	895	7	CF552020	CF552020 AGENCOURT
	18	864.4	32.5	949	5	BX423078	BX423078 BX423078
c	19	863.4	32.4	1011	5	BX406948	BX406948 BX406948
c	20	862.2	32.4	905	1	AL542811	AL542811 AL542811
c	21	851.2	32.0	930	5	BX364870	BX364870 BX364870
	22	844.6	31.7	987	5	BX381217	BX381217 BX381217
c	23	835.4	31.4	1035	1	AL575920	AL575920 AL575920
c	24	827.2	31.1	957	5	BX396828	BX396828 BX396828
	25	823	30.9	858	1	AL542812	AL542812 AL542812
	26	816.6	30.7	891	5	BX452668	BX452668 BX452668
	27	815.8	30.7	911	4	BI521316	BI521316 603081887
	28	799.8	30.1	910	5	BX396829	BX396829 BX396829
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	30	788	29.6	1107	4	BM550298	BM550298 AGENCOURT
	31	779	29.3	1089	4	BM547872	BM547872 AGENCOURT
	32	776	29.2	835	4	BG576651	BG576651 602597538
	33	775	29.1	808	4	BG742272	BG742272 602631402
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	35	758.2	28.5	810	1	AU139997	AU139997 AU139997
c	36	749.8	28.2	993	1	AL564958	AL564958 AL564958
	37	745	28.0	754	4	BG211992	BG211992 RST31703
	38	743.8	28.0	892	5	BU157659	BU157659 AGENCOURT
c	39	742.4	27.9	878	5	BX437190	BX437190 BX437190
	40	737.8	27.7	855	5	BU178305	BU178305 AGENCOURT

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<div align="center">ALIGNMENTS</div>

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RESULT 1
BC025297
LOCUS       BC025297                2636 bp    mRNA    linear   HTC 08-MAR-2002
DEFINITION  Homo sapiens, glycoprotein (transmembrane) nmb, clone
            IMAGE:4877773, mRNA.
ACCESSION   BC025297
VERSION     BC025297.1  GI:19264140
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2636)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
            Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
            Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
            Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
            Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
            Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
            George Yang, Scott Zuyderduyn, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 42 Row: i Column: 5
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4505404
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
     source          1. .2636
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                     /mol_type="mRNA"
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                    /db_xref="taxon:9606"
                    /clone="IMAGE:4877773"
                    /tissue_type="Skin, melanotic melanoma, high MDR."
                    /clone_lib="NIH_MGC_49"
                    /lab_host="DH10B-R"
                    /note="Vector: pOTB7"
ORIGIN

  Query Match                95.8%;  Score 2550;  DB 3;  Length 2636;
  Best Local Similarity      99.1%;  Pred. No. 0;
  Matches 2595;  Conservative    0;  Mismatches   20;  Indels    3;  Gaps    3;

Qy       28 AACCTTGGTGCCTGCGTCCGTGAGAATTCAGCATGGAATGTCTCTACTATTTCCTGGGAT 87
            |  |  |   |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       20 ACCTTGAGTGCCTGCGTCCGTGAGAATTCAGCATGGAATGTCTCTACTATTTCCTGGGAT 79

Qy       88 TTCTGCTCCTGGCTGCAAGATTGCCACTTGATGCCGCCAAACGATTTCATGATGTGCTGG 147
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       80 TTCTGCTCCTGGCTGCAAGATTGCCACTTGATGCCGCCAAACGATTTCATGATGTGCTGG 139

Qy      148 GCAATGAAAGACCTTCTGCTTACATGAGGGAGCACAATCAATTAAATGGCTGGTCTTCTG 207
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Db      140 GCAATGAAAGACCTTCTGCTTACATGAGGGAGCACAATCAATTAAATGGCTGGTCTTCTG 199

Qy      208 ATGAAAATGACTGGAATGAAAAACTCTACCCAGTGTGGAAGCGGGGAGACATGAGGTGGA 267
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Qy      388 CCAATGGCAACATAGTCTATGAGAAGAACTGCAGAAATGAGGCTGGTTTATCTGCTGATC 447
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      380 CCAATGGCAACATAGTCTATGAGAAGAACTGCAGAAATGAGGCTGGTTTATCTGCTGATC 439

Qy      448 CATATGTTTACAACTGGACAGCATGGTCAGAGGACAGTGACGGGGAAAATGGCACCGGCC 507
            | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      440 CGTATGTTTACAACTGGACAGCATGGTCAGAGGACAGTGACGGGGAAAATGGCACCGGCC 499

Qy      508 AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCCGGATGGAGAA 567
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      500 AAAGCCATCATAACGTCTTCCCTGATGGGAAACCTTTTCCTCACCACCCCGGATGGAGAA 559

Qy      568 GATGGAATTTCATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGAT 627
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      560 GATGGAATTTCATCTACGTCTTCCACACACTTGGTCAGTATTTCCAGAAATTGGGACGAT 619

Qy      628 GTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG 687
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      620 GTTCAGTGAGAGTTTCTGTGAACACAGCCAATGTGACACTTGGGCCTCAACTCATGGAAG 679
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Qy     688 TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGT 747
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     680 TGACTGTCTACAGAAGACATGGACGGGCATATGTTCCCATCGCACAAGTGAAAGATGTGT 739

Qy     748 ACGTGGTAACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT 807
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ⁻
Db     740 ACGTGGTAACAGATCAGATTCCTGTGTTTGTGACTATGTTCCAGAAGAACGATCGAAATT 799

Qy     808 CATCCGACGAAACCTTCC-CAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC 866
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     800 CATCCGACGAAACCTTCCTCAAAGATCTCCCCATTATGTTTGATGTCCTGATTCATGATC 859

Qy     867 CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTG 926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     860 CTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGAGCTTCGGGGATAATACTG 919

Qy     927 GCCTGTTTGTTTCCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGAACCTTCA 986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     920 GCCTGTTTGTTTCCACCAATCATACTGTGAATCACACGTATGTGCTCAATGGAACCTTCA 979

Qy     987 GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCCACCGCCACCACCAC 1046
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     980 GCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCCACCGCCACCACCAC 1039

Qy    1047 CCAGACCTTCAAAACCCACCCCTTCTTTAGGACCTGCTGGTGACAACCCCCTGGAGCTGA 1106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1040 CCAGACCTTCAAAACCCACCCCTTCTTTAGGACCTGCTGGTGACAACCCCCTGGAGCTGA 1099

Qy    1107 GTAGGATTCCTGATGAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCA 1166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1100 GTAGGATTCCTGATGAAAACTGCCAGATTAACAGATATGGCCACTTTCAAGCCACCATCA 1159

Qy    1167 CAATTGTAGAGGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCCTGATGCCGG 1226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1160 CAATTGTAGAGGGAATCTTAGAGGTTAACATCATCCAGATGACAGACGTCCTGATGCCGG 1219

Qy    1227 TGCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCCA 1286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1220 TGCCATGGCCTGAAAGCTCCCTAATAGACTTTGTCGTGACCTGCCAAGGGAGCATTCCCA 1279

Qy    1287 CGGAGGTCTGTACCATCATTTCTGACCCCACCTGCGAGATCACCCAGAACACAGTCTGCA 1346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1280 CGGAGGTCTGTACCATCATTTCTGACCCCACCTGCGAGATCACCCAGAACACAGTCTGCA 1339

Qy    1347 GCCCTGTGGATGTGGATGAGATGTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTG 1406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1340 GCCCTGTGGATGTGGATGAGATGTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTG 1399

Qy    1407 GGACGTACTGTGTGAACCTCACCCTGGGGGATGACACAAGCCTGGCTCTCACGAGCACCC 1466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1400 GGACGTACTGTGTGAACCTCACCCTGGGGGATGACACAAGCCTGGCTCTCACGAGCACCC 1459

Qy    1467 TGATTTCTGTTCCTGACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGA 1526
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1460 TGATTTCTGTTCCTGACAGAGACCCAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGA 1519

Qy    1527 TCTCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTGGTGTACAAAAAAC 1586
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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1520 TCTCCGTTGGCTGCTTGGCCATATTTGTCACTGTGATCTCCCTCTTGGTGTACAAAAAC 1579

Qy    1587 ACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGTGGTCAGAAGCAAAGGCCTGA 1646
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1580 ACAAGGAATACAACCCAATAGAAAATAGTCCTGGGAATGTGGTCAGAAGCAAAGGCCTGA 1639

Qy    1647 GTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTTCCCGGGAAACCAGGAAAAGGATCCGC 1706
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1640 GTGTCTTTCTCAACCGTGCAAAAGCCGTGTTCTTCCCGGGAAACCAGGAAAAGGATCCGC 1699

Qy    1707 TACTCAAAAACCAAGAATTTAAAGGAGTTTCTTAAATTTCGACCTTGTTTCTGAAGCTCA 1766
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1700 TACTCAAAAACCAAGAATTTAAAGGAGTTTCTTAAATTTCGACCTTGTTTCTGAAGCTCA 1759

Qy    1767 CTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTGGCTATTAACCTTTTTTTCCTAAAG 1826
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1760 CTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTGGCTATTAACCTTTTTTTCCTAAAG 1819

Qy    1827 ATTATTGTTAAATAGATATTGTGGTTTGGGGAAGTTGAATTTTTTATAGGTTAAATGTCA 1886
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1820 ATTATTGTTAAATAGATATTGTGGTTTGGGGAAGTTGAATTTTTTATAGGTTAAATGTCA 1879

Qy    1887 TTTTAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTCAGCCATGTTGTGAAACTGAT 1946
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1880 TTTTAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTCAGCCATGTTGTGAAACTGAT 1939

Qy    1947 AAAAGCAACTTAGCAAGGCTTCTTTTCATTATTTTTTATGTTTCACTTATAAAGTCTTAG 2006
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1940 AAAAGCAACTTAGCAAGGCTTCTTTTCATTATTTTTTATGTTTCACTTATAAAGTCTTAG 1999

Qy    2007 GTAACTAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAGAAGCTACTATTGATTA 2066
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2000 GTAACTAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAGAAGCTACTATTGATTA 2059

Qy    2067 GAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGGGATACTTTCAGCTTTCCATGTAACTG 2126
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2060 GAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGGGATACTTTCAGCTTTCCATGTAACTG 2119

Qy    2127 TATGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCA 2186
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2120 TATGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTAACTGAATCCCA 2179

Qy    2187 CTTCAATACACACTCATGAACTCCTGATGGAACAATAACAGGCCCAAGCCTGTGGTATGA 2246
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2180 CTTCAATACACACTCATGAACTCCTGATGGAACAATAACAGGCCCAAGCCTGTGGTATGA 2239

Qy    2247 TGTGCACACTTGCTAGACTCAGAAAAAATACTACTCTCATAAATGGGTGGGAGTATTTTG 2306
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2240 TGTGCACACTTGCTAGACTCAGAAAAAATACTACTCTCATAAATGGGTGGGAGTATTTTG 2299

Qy    2307 GTGACAACCTACTTTGCTTGGCTGAGTGAAGGAATGATATTCATATATTCATTTATTCCA 2366
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2300 GTGACAACCTACTTTGCTTGGCTGAGTGAAGGAATGATATTCATATATTCATTTATTCCA 2359

Qy    2367 TGGACATTTAGTTAGTGCTTTTTATATACCAGGCATGATGCTGAGTGACACTCTTGTGTA 2426
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    2360  TGGACATTTAGTTAGTGCTTTTTATATACCAGGCATGATGCTGAGTGACACTCTTGTGTA  2419

Qy    2427  TATTTCCAAATTTTTGTATAGTCGCTGCACATATTTGAAATCAAAATATTAAGACTTTCC  2486
            |||||||||||||||||| |||||||||||||||||||||||| | |||||||||||||||
Db    2420  TATTTCCAAATTTTTGTACAGTCGCTGCACATATTTGAAATC-ATATATTAAGACTTTCC  2478

Qy    2487  AAAAATTTGGTCCCTGGTTTTTCATGGCAACTTGATCAGTAAGGATTTCCCCTCTGTTTG  2546
            ||| ||  ||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    2479  AAAGATGAGGTCCCTGGTTTTTCATGGCAACTTGATCAGTAAGGATTTCACCTCTGTTTG  2538

Qy    2547  GAACTAAAACCATTTACTATATGTTAGACAAGACATTTTTTTTTTTCCTTCCTGAAAAA  2606
            ||||||||||||| |||||||||||||||| ||||||| ||||| | |||||||||||||
Db    2539  TAACTAAAACCATCTACTATATGTTAGACATGACATTCTTTTTCTCTCCTTCCTGAAAAA  2598

Qy    2607  -AAAATGAGGGAAGAGACAAAAAAAAAAAAAAAAAAAAAAA  2643
            ||| || |||||||||||||||||||||||||||||||||
Db    2599  TAAAGTGTGGGAAGAGACAAAAAAAAAAAAAAAAAAAAAAA  2636
```

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 18, 2005, 22:03:33 ; Search time 355 Seconds
                                     (without alignments)
                                     5798.137 Million cell updates/sec

Title: US-10-039-272-1
Perfect score: 4850
Sequence: 1 cggcacgagggcccagagga.........aaaaaaaaaaaaaaaaaaaa 2661

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop   6.0 , Delext   7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10039272/runat_18022005_095204_14690/app_query.fasta_1
.2823
-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10039272_@CGN_1_1_398_@runat_18022005_095204_14690 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   A_Geneseq_16Dec04:*
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*

        Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3014	62.1	563	8	ADR66659	Adr66659 Human pro
2	3014	62.1	563	8	ADR66317	Adr66317 Human pro
3	3014	62.1	563	8	ADR66339	Adr66339 Human pro
4	3014	62.1	563	8	ADR66681	Adr66681 Human pro
5	2999	61.8	560	2	AAW35382	Aaw35382 Murine me
6	2999	61.8	560	3	AAB11329	Aab11329 Human lun
7	2999	61.8	560	5	ABB78200	Abb78200 Amino aci
8	2999	61.8	560	5	ABB74961	Abb74961 Human lun
9	2999	61.8	560	5	ABP61881	Abp61881 Human lun
10	2999	61.8	560	6	ABU56592	Abu56592 Lung canc
11	2999	61.8	560	6	ABG72962	Abg72962 Human ost
12	2999	61.8	560	6	ABU70852	Abu70852 Human adi
13	2999	61.8	560	7	ADA28315	Ada28315 Human lun
14	2999	61.8	560	7	ADE95620	Ade95620 Human NOV
15	2999	61.8	560	7	ADH36879	Adh36879 Human lun
16	2999	61.8	560	7	ADJ68660	Adj68660 Human hea
17	2999	61.8	560	7	ADL14995	Adl14995 Human NMB
18	2999	61.8	560	7	ADN39940	Adn39940 Cancer/an
19	2999	61.8	560	8	ADH56342	Adh56342 Human nmb
20	2999	61.8	560	8	ADJ75569	Adj75569 Marker ge
21	2999	61.8	560	8	ADM56682	Adm56682 Human lun
22	2999	61.8	560	8	ADQ18310	Adq18310 Human sof
23	2999	61.8	560	8	ADP23127	Adp23127 PRO polyp
24	2980	61.4	572	7	ADD78235	Add78235 Human CGD
25	2979	61.4	572	5	AAU83612	Aau83612 Human PRO
26	2979	61.4	572	6	ABU80759	Abu80759 Human PRO
27	2979	61.4	572	6	ABO33725	Abo33725 Novel hum
28	2979	61.4	572	6	ABU82068	Abu82068 Novel hum
29	2979	61.4	572	6	ABJ72248	Abj72248 Human PRO
30	2979	61.4	572	6	ABJ72376	Abj72376 Human PRO
31	2979	61.4	572	6	ABO34271	Abo34271 Human sec
32	2979	61.4	572	7	ABJ72078	Abj72078 Human mem
33	2979	61.4	572	7	ADB83532	Adb83532 Novel hum
34	2979	61.4	572	7	ADB80638	Adb80638 Novel hum
35	2979	61.4	572	7	ADB73179	Adb73179 Novel hum
36	2979	61.4	572	7	ADB78261	Adb78261 Novel hum
37	2979	61.4	572	7	ADB84909	Adb84909 Human PRO
38	2979	61.4	572	7	ADB78015	Adb78015 Novel hum
39	2979	61.4	572	7	ADB87081	Adb87081 Human PRO
40	2979	61.4	572	7	ADB84663	Adb84663 Human PRO
41	2979	61.4	572	7	ADB83778	Adb83778 Novel hum
42	2979	61.4	572	7	ADB72933	Adb72933 Novel hum
43	2979	61.4	572	7	ADC36771	Adc36771 Human PRO
44	2979	61.4	572	7	ADC21761	Adc21761 Human PRO
45	2979	61.4	572	7	ADC49792	Adc49792 Novel hum

GenCore version 5.1.6

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 18, 2005, 22:15:00 ; Search time 73 Seconds
                                        (without alignments)
                                        5442.224 Million cell updates/sec

Title: US-10-039-272-1
Perfect score: 4850
Sequence: 1 cggcacgagggcccagagga.........aaaaaaaaaaaaaaaaaaaa 2661

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10039272/runat_18022005_095206_14721/app_query.fasta_1
.2823
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10039272_@CGN_1_1_72_@runat_18022005_095206_14721 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2999	61.8	560	1	US-09-985-799-90	Sequence 90, Appl
2	2999	61.8	560	1	US-09-977-371-90	Sequence 90, Appl
3	2999	61.8	560	1	US-08-594-031-90	Sequence 90, Appl
4	2999	61.8	560	4	US-09-643-597-225	Sequence 225, App
5	2999	61.8	560	4	US-09-480-884A-225	Sequence 225, App
6	2999	61.8	560	4	US-09-542-615A-225	Sequence 225, App
7	2999	61.8	560	4	US-09-606-421B-225	Sequence 225, App
8	2999	61.8	560	4	US-09-476-496A-225	Sequence 225, App
9	2999	61.8	560	4	US-09-630-940B-225	Sequence 225, App
10	2999	61.8	560	4	US-09-943-075A-6	Sequence 6, Appli
11	2170	44.7	574	3	US-09-383-586-36	Sequence 36, Appl
12	2170	44.7	574	4	US-09-823-038A-36	Sequence 36, Appl
13	2170	44.7	574	4	US-09-943-075A-5	Sequence 5, Appli
14	2152	44.4	572	4	US-09-197-970B-5	Sequence 5, Appli
15	2136	44.0	572	4	US-09-943-075A-2	Sequence 2, Appli
16	950.5	19.6	376	1	US-09-985-799-100	Sequence 100, App
17	950.5	19.6	376	1	US-09-985-799-102	Sequence 102, App
18	950.5	19.6	376	1	US-09-977-371-100	Sequence 100, App
19	950.5	19.6	376	1	US-09-977-371-102	Sequence 102, App
20	950.5	19.6	376	1	US-08-594-031-100	Sequence 100, App
21	950.5	19.6	376	1	US-08-594-031-102	Sequence 102, App
22	593	12.2	661	2	US-08-417-174-121	Sequence 121, App
23	593	12.2	661	3	US-09-267-439-121	Sequence 121, App
24	593	12.2	661	4	US-08-388-852B-2	Sequence 2, Appli
25	593	12.2	661	4	US-09-073-138-121	Sequence 121, App
26	592	12.2	661	2	US-08-417-174-27	Sequence 27, Appl
27	592	12.2	661	2	US-08-231-565A-27	Sequence 27, Appl
28	592	12.2	661	2	US-09-007-961-27	Sequence 27, Appl
29	592	12.2	661	3	US-09-267-439-27	Sequence 27, Appl
30	592	12.2	661	4	US-09-073-138-27	Sequence 27, Appl
31	574.5	11.8	668	1	US-07-891-942G-6	Sequence 6, Appli
32	327.5	6.8	460	4	US-09-949-016-8029	Sequence 8029, Ap
33	238.5	4.9	190	4	US-08-388-852B-35	Sequence 35, Appl
34	236	4.9	202	4	US-08-388-852B-38	Sequence 38, Appl
35	233.5	4.8	192	4	US-08-388-852B-37	Sequence 37, Appl
36	233	4.8	197	4	US-08-388-852B-36	Sequence 36, Appl
37	124	2.6	71	1	US-09-985-799-98	Sequence 98, Appl
38	124	2.6	71	1	US-09-977-371-98	Sequence 98, Appl
39	124	2.6	71	1	US-08-594-031-98	Sequence 98, Appl
40	120	2.5	724	4	US-09-784-358-8	Sequence 8, Appli
41	120	2.5	845	4	US-09-784-358-12	Sequence 12, Appl
42	120	2.5	1691	4	US-09-784-358-2	Sequence 2, Appli
43	112.5	2.3	440	4	US-09-248-796A-26860	Sequence 26860, A
44	111	2.3	525	4	US-09-976-594-64	Sequence 64, Appl
45	111	2.3	525	4	US-09-919-039-62	Sequence 62, Appl

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OM nucleic - protein search, using frame_plus_n2p model

```
Run on:              February 18, 2005, 22:44:56 ; Search time 303.5 Seconds
                                                    (without alignments)
                                                    5738.309 Million cell updates/sec

Title:               US-10-039-272-1
Perfect score:       4850
Sequence:            1 cggcacgagggcccagagga..........aaaaaaaaaaaaaaaaaaaa 2661

Scoring table:       BLOSUM62
                     Xgapop 10.0 , Xgapext  0.5
                     Ygapop 10.0 , Ygapext  0.5
                     Fgapop  6.0 , Fgapext  7.0
                     Delop   6.0 , Delext   7.0

Searched:            1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters:       2760536

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10039272/runat_18022005_095208_14781/app_query.fasta_1
.2823
-DB=Published_Applications_AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10039272_@CGN_1_1_393_@runat_18022005_095208_14781
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :           Published_Applications_AA:*
                     1:   /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                     2:   /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                     3:   /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                     4:   /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                     5:   /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                     6:   /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                     7:   /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                     8:   /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                     9:   /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                     10:  /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                     11:  /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                     12:  /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                     13:  /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                     14:  /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                     15:  /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                     16:  /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
```

```
        17:   /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
        18:   /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
        19:   /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
        20:   /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                     SUMMARIES
                      %
     Result        Query
       No.   Score  Match Length DB  ID                       Description
     -----------------------------------------------------------------------
         1    2999   61.8    560   9  US-09-735-705-225       Sequence 225, App
         2    2999   61.8    560   9  US-09-850-716A-225      Sequence 225, App
         3    2999   61.8    560   9  US-09-897-778-225       Sequence 225, App
         4    2999   61.8    560   9  US-09-943-075A-6        Sequence 6, Appli
         5    2999   61.8    560  13  US-10-039-272-2         Sequence 2, Appli
         6    2999   61.8    560  14  US-10-007-700-225       Sequence 225, App
         7    2999   61.8    560  14  US-10-117-982-225       Sequence 225, App
         8    2999   61.8    560  15  US-10-463-106-2         Sequence 2, Appli
         9    2999   61.8    560  15  US-10-295-027-1258      Sequence 1258, Ap
        10    2999   61.8    560  15  US-10-313-986-225       Sequence 225, App
        11    2999   61.8    560  15  US-10-309-290-152       Sequence 152, App
        12    2999   61.8    560  16  US-10-408-765A-466      Sequence 466, App
        13    2979   61.4    572  14  US-10-227-884-42        Sequence 42, Appl
        14    2979   61.4    572  14  US-10-230-163-42        Sequence 42, Appl
        15    2979   61.4    572  14  US-10-230-338-42        Sequence 42, Appl
        16    2979   61.4    572  14  US-10-218-631-42        Sequence 42, Appl
        17    2979   61.4    572  14  US-10-230-414-42        Sequence 42, Appl
        18    2979   61.4    572  14  US-10-232-224-42        Sequence 42, Appl
        19    2979   61.4    572  14  US-10-216-159A-42       Sequence 42, Appl
        20    2979   61.4    572  14  US-10-218-849-42        Sequence 42, Appl
        21    2979   61.4    572  14  US-10-227-873-42        Sequence 42, Appl
        22    2979   61.4    572  14  US-10-227-883-42        Sequence 42, Appl
        23    2979   61.4    572  14  US-10-219-076-42        Sequence 42, Appl
        24    2979   61.4    572  14  US-10-230-434-42        Sequence 42, Appl
        25    2979   61.4    572  14  US-10-219-003-42        Sequence 42, Appl
        26    2979   61.4    572  14  US-10-219-075-42        Sequence 42, Appl
        27    2979   61.4    572  14  US-10-219-464-42        Sequence 42, Appl
        28    2979   61.4    572  14  US-10-219-466-42        Sequence 42, Appl
        29    2979   61.4    572  14  US-10-219-479-42        Sequence 42, Appl
        30    2979   61.4    572  14  US-10-219-481-42        Sequence 42, Appl
        31    2979   61.4    572  14  US-10-230-260-42        Sequence 42, Appl
        32    2979   61.4    572  14  US-10-232-231-42        Sequence 42, Appl
        33    2979   61.4    572  14  US-10-232-233-42        Sequence 42, Appl
        34    2979   61.4    572  14  US-10-216-165-42        Sequence 42, Appl
        35    2979   61.4    572  14  US-10-218-956-42        Sequence 42, Appl
        36    2979   61.4    572  14  US-10-219-468-42        Sequence 42, Appl
        37    2979   61.4    572  14  US-10-219-478-42        Sequence 42, Appl
        38    2979   61.4    572  14  US-10-219-536-42        Sequence 42, Appl
        39    2979   61.4    572  14  US-10-233-205-42        Sequence 42, Appl
        40    2979   61.4    572  14  US-10-219-072-42        Sequence 42, Appl
        41    2979   61.4    572  14  US-10-219-470-42        Sequence 42, Appl
        42    2979   61.4    572  14  US-10-219-474-42        Sequence 42, Appl
        43    2979   61.4    572  14  US-10-219-524-42        Sequence 42, Appl
```

```
44    2979    61.4    572  14   US-10-219-528-42          Sequence 42, Appl
45    2979    61.4    572  14   US-10-227-880-42          Sequence 42, Appl
```

<div align="center">

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</div>

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 18, 2005, 22:06:53 ; Search time 91 Seconds
                                          (without alignments)
                                          5627.095 Million cell updates/sec

Title: US-10-039-272-1
Perfect score: 4850
Sequence: 1 cggcacgagggcccagagga..........aaaaaaaaaaaaaaaaaaaa 2661

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10039272/runat_18022005_095205_14708/app_query.fasta_1
.2823
-DB=PIR_79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10039272_@CGN_1_1_135_@runat_18022005_095205_14708 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   PIR_79:*
                  1: pir1:*
                  2: pir2:*
                  3: pir3:*
                  4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2999	61.8	560	2	I38065	gene NMB protein -
2	635	13.1	626	2	S53871	Pmel 17 protein -
3	593.5	12.2	662	2	I38400	melanoma-associate
4	588.5	12.1	668	2	A41234	melanocyte-specifi
5	436.5	9.0	491	2	A49179	melanoma antigen h
6	135	2.8	446	2	T07907	hydroxyproline-ric
7	129	2.7	926	1	A41105	protein-tyrosine-p
8	118	2.4	2869	2	T18518	apolipoprotein(a)
9	116.5	2.4	555	2	S21766	dihydrolipoamide S
10	114	2.4	2395	1	S50820	surface protein ty
11	113	2.3	1541	2	T02831	AAA protein L4171.
12	112.5	2.3	457	2	I55976	dihydrolipoamide S
13	111.5	2.3	2946	2	T15840	hypothetical prote
14	111	2.3	525	1	KGHUGH	histidine-rich gly
15	110.5	2.3	1874	1	JQ0533	genome polyprotein
16	109.5	2.3	492	2	C96521	protein F21D18.18
17	109	2.2	1737	2	A59235	unconventional myo
18	108.5	2.2	348	2	AB3260	hypothetical membr
19	108.5	2.2	588	2	T45564	hypothetical prote
20	107.5	2.2	768	2	A87722	protein ZC123.1 [i
21	107.5	2.2	1208	2	T27822	hypothetical prote
22	106	2.2	658	2	T08153	cysteine proteinas
23	106	2.2	1537	2	S53465	flocculation prote
24	106	2.2	1585	2	T31611	hypothetical prote
c 25	105	2.2	499	2	S52422	chitinase (EC 3.2.
26	104.5	2.2	4006	2	T09070	probable tenascin
27	104	2.1	435	2	D41602	transcription fact
28	103	2.1	626	1	NBHUIA	platelet glycoprot
29	103	2.1	921	2	A33718	retinoblastoma pro
30	103	2.1	1009	2	C64483	hypothetical prote
c 31	102.5	2.1	394	2	E82572	ABC transporter so
32	102.5	2.1	826	2	G90283	hypothetical prote
33	102.5	2.1	979	2	A35913	regulatory factor
34	102	2.1	281	2	T29150	hypothetical prote
35	102	2.1	393	2	T33103	lin-1 protein - Ca
36	102	2.1	1213	2	A41724	limb deformity (ld
37	102	2.1	2014	2	T21560	hypothetical prote
38	101.5	2.1	445	2	D81716	hypothetical prote
39	101.5	2.1	2165	2	T21371	hypothetical prote
40	101	2.1	848	2	T23694	hypothetical prote
41	101	2.1	2090	2	S26058	probable transform
42	100.5	2.1	221	2	T07176	extensin homolog -
43	100.5	2.1	1048	2	T30815	platelet-derived g
44	100	2.1	432	2	AB2222	twitching motility
45	100	2.1	26926	1	I38344	titin, cardiac mus

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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 18, 2005, 22:04:28 ; Search time 445 Seconds
                                        (without alignments)
                                        6124.237 Million cell updates/sec

Title: US-10-039-272-1
Perfect score: 4850
Sequence: 1 cggcacgagggcccagagga.........aaaaaaaaaaaaaaaaaaaa 2661

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10039272/runat_18022005_095205_14696/app_query.fasta_1
.2823
-DB=UniProt_03 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10039272_@CGN_1_1_518_@runat_18022005_095205_14696 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   UniProt_03:*
                  1: uniprot_sprot:*
                  2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                             SUMMARIES
                        %
Result   Query
  No.   Score Match Length DB   ID   Description

1	2999	61.8	560	1	NMB_HUMAN	Q14956	homo sapien
2	2983	61.5	572	2	Q8N1A1	Q8n1a1	homo sapien
3	2979	61.4	572	2	Q6UVX1	Q6uvx1	homo sapien
4	2170	44.7	574	2	Q99P91	Q99p91	mus musculu
5	2170	44.7	574	2	Q8BVV9	Q8bvv9	mus musculu
6	2170	44.7	574	2	Q9QXA0	Q9qxa0	mus musculu
7	2166	44.7	574	2	Q8BXL4	Q8bxl4	mus musculu
8	2152	44.4	572	2	Q6P7C7	Q6p7c7	rattus norv
9	2136	44.0	572	2	Q9QZF6	Q9qzf6	rattus norv
10	2015	41.5	526	2	Q8BVA0	Q8bva0	mus musculu
11	1563.5	32.2	559	1	QNR_COTJA	Q90372	coturnix co
12	1029	21.2	206	2	Q96F58	Q96f58	homo sapien
13	1022	21.1	206	2	Q8IXJ5	Q8ixj5	homo sapien
14	711.5	14.7	721	2	Q6DDN6	Q6ddn6	xenopus lae
15	704.5	14.5	746	2	Q6DIR2	Q6dir2	xenopus tro
16	644.5	13.3	626	2	Q9CZB2	Q9czb2	mus musculu
17	635	13.1	626	1	PM17_MOUSE	Q60696	mus musculu
18	631.5	13.0	760	2	Q6DW64	Q6dw64	gallus gall
19	630	13.0	733	2	O93391	O93391	coturnix co
20	629.5	13.0	764	2	Q6DW63	Q6dw63	gallus gall
21	628	12.9	763	2	Q6DW62	Q6dw62	gallus gall
22	620.5	12.8	788	2	Q6DW65	Q6dw65	gallus gall
23	617	12.7	762	1	P115_CHICK	Q98917	gallus gall
24	612	12.6	783	2	Q6DW60	Q6dw60	gallus gall
25	609	12.6	759	2	Q6DW61	Q6dw61	gallus gall
26	593	12.2	661	1	PM17_HUMAN	P40967	homo sapien
27	436.5	9.0	491	1	PM17_BOVIN	Q06154	bos taurus
28	372	7.7	461	2	O97884	O97884	equus cabal
29	247.5	5.1	236	2	Q9QY67	Q9qy67	mus musculu
30	198.5	4.1	423	2	Q8N0W9	Q8n0w9	homo sapien
31	198.5	4.1	435	2	Q8N3G9	Q8n3g9	homo sapien
32	192	4.0	397	2	Q8N3R2	Q8n3r2	homo sapien
33	167	3.4	141	2	Q9QY70	Q9qy70	mus musculu
34	154.5	3.2	419	2	Q6NXM3	Q6nxm3	mus musculu
35	151	3.1	354	2	Q8IY46	Q8iy46	homo sapien
36	141.5	2.9	906	2	Q8TPY9	Q8tpy9	methanosarc
37	135	2.8	446	2	O22458	O22458	chlamydomon
38	134.5	2.8	1817	2	Q8TI59	Q8ti59	methanosarc
39	131	2.7	879	2	Q8PWJ6	Q8pwj6	methanosarc
40	129.5	2.7	1131	2	Q75DJ5	Q75dj5	ashbya goss
41	129	2.7	926	1	PTN4_HUMAN	P29074	homo sapien
42	128.5	2.6	688	2	Q8TR88	Q8tr88	methanosarc
43	127.5	2.6	3988	2	Q8TPZ1	Q8tpz1	methanosarc
44	126	2.6	603	2	Q7U5X8	Q7u5x8	synechococc
45	125.5	2.6	881	2	Q6H7U3	Q6h7u3	oryza sativ